

GeneCore version 5.1.6
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CM nucleic - nucleic search, using SW model

Run on:

August 24, 2004, 17:45:39 ; Search time 4175 Seconds

(without alignments)

6623.439 Million cell updates/sec

Title: US-10-022-554A-3

Perfect score: 1.98578 seqe, 21671516995 residues

Searched:

Total number of hits satisfying chosen parameters: 6940544

Scoring table: IDENTI_WRC

Scoring table: GapOp 10.0, GapExt 1.0

Maximum DB seq length: 0 Maximum Match 100%

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database: GenBank

1: gb_bai*
2: gb_htg*
3: gb_jin*
4: gb_om*
5: gb_ovr*
6: gb_pati*
7: gb_jhu*
8: gb_pdi*
9: gb_prt*
10: gb_ror*
11: gb_sar*
12: gb_syr*
13: gb_uni*
14: gb_v1*
15: em_bai*
16: em_fun*
17: em_hum*
18: em_in*
19: em_mus*
20: em_on*
21: em_oxi*
22: em_pat*
24: em_ph*
25: em_P1*
26: em_ror*
27: em_stc*
28: em_ua*
29: em_v1*
30: em_htg_hum*
31: em_htg_inv*
32: em_htg_other*
33: em_htg_mus*
34: em_tg_p1*
35: em_htg_ror*
36: em_htg_mam*
37: em_htg_vrt*
38: em_BY*
39: em_htg_hum*
40: em_htg_mus*
41: em_htg_othe*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

QY

Query Match 99.2t; Score 633.7; DB 6; Length 638;

Best Local Similarity 99.5%; Pred. No. 7.9e-149; Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1	633.2	99.2	638	6	I02042 Sequence 5
2	633.2	99.2	638	6	I08496 Sequence 7
3	633.2	99.2	638	9	M1361 Human beta-cetobutyrate kinase
4	601.4	94.3	10713	9	BC012617 Homo sapiens
5	601.4	94.3	2259	9	X51943 Human mRNA
6	549.8	86.2	638	6	I08090 Sequence 4
7	549.8	86.2	638	6	I01338 Sequence 3
8	491.8	77.1	405	4	BTGP08R Sequence
9	485.2	76.1	490	6	AK28045 Sequence
10	485.2	76.1	490	9	HSKAGE
11	474.2	74.3	668	4	BOVGPRA
12	474.2	74.3	668	4	BTIDGE
13	470.6	73.8	8501	6	AK4920 Sequence
14	464	72.7	481	6	X13221 Bovine mRNA
15	464	72.7	102297	6	AK33085 Sequence
16	463.2	72.6	458	6	X65778 H. sapiens a
17	463.2	72.6	AK81449	6	M35018 Bovine acid
18	460	72.1	496	6	X140328 Bovine mRNA
19	459.2	72.1	496	6	A00329 Artificial
20	459.2	72.1	567291	6	S67791 Homo sapiens
21	434.6	68.1	2440	10	BC031601
22	434.6	68.1	102297	10	MK061610
23	432	67.7	1216	10	RHBBP1
24	422.4	66.2	472	4	SSA9GRNA
25	412.8	64.7	454	6	A00059 Artificial
26	412.8	64.7	454	6	A00070 Artificial
27	412.8	64.7	454	6	A02757 DNA
28	412.8	64.7	454	6	BC031601
29	412.8	64.7	454	6	BD0343 cDNA
30	412.8	64.7	454	6	BD0352 cDNA
31	412.8	64.7	454	6	BD0557 Human arof
32	412.8	64.7	454	6	AR32520 Sequence
33	400.2	62.7	537	6	E3B005 Process for
34	397.8	62.4	610	6	E2B527
35	397.6	62.3	537	6	E3B005 Process for
36	397.4	62.3	516	6	E3B5025
37	397.2	62.3	408	6	E37983 Process for
38	397.2	62.3	516	6	E2B510 Sugar chain
39	397.2	62.3	525	6	E37984 Process for
40	397.2	62.3	525	6	E2B522 Sugar chain
41	397.2	62.3	600	6	E2B522
42	397.2	62.3	600	6	E2B523 Sugar chain
43	397.2	62.3	653	6	E2B509 Sugar chain
44	397.2	62.3	653	6	E2B524 Sugar chain
45	397.2	62.3	843	6	E2B525 Sugar chain

ALIGNMENTS

RESULT 1
102042

LOCUS 102042 Sequence 5 from Patent: US 4868113.

DEFINITION Human endothelial cell growth

ACCESSION 102042

VERSION 10.2042.1 GI:270417

KEYWORDS

ORGANISM Unknown.

Unclassified.

REFERENCE 1. (bases 1 to 638)

AUTHORS Jaye, M., Burgess, N., Maciag, T. and Drohan, W.

TITLE Recombinant DNA vector encoding human endothelial cell growth

factor

Patent, US 4868113-A 5-19-SEP-1999;

JOURNAL Rorer Biotechnology, Inc.; King of Prussia, PA

FEATURES Location/Qualifiers

source 1. -638 /organism="Unknown"

/mol_type="unassigned DNA"

ORIGIN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Genoscope - Centre National de Séquençage
BP 131 91065 EVRY cedex - France
Email: secrete@genoscope.cnrs.fr. Web : www.genoscope.cnrs.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3201.r. For
more information about this cluster, see
<http://www.genoscope.cnrs.fr/cgi-bin/clustal.cgi?seq=CS003D938Q1cluster=3201.r>. Contact:
Feng Liang Email: Fliang@itetc.com URL:
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID: CS003D938Q1

			Location/Qualifiers
1	501..8	94..3	1173 13 BX444567
2	576..9	90..4	832 12 BX444567
3	569..4	89..2	816 9 BX69731 603193620
4	567..9	88..7	1057 13 BQ687949
5	560..8	87..9	1014 12 BM09005
6	559..8	87..7	872 12 B1593845
7	511..4	80..2	821 12 B1598930
8	501..6	78..6	534 9 A1590078 tcm5801..
9	437..6	68..6	714 12 A1590078 tcm5801..
10	434..6	68..1	472 9 A1076909
11	425..4	66..7	3404 11 AX035330
12	424..2	65..5	843 12 B1592283
13	420..6	65..9	461 10 BPP56665
14	408..2	64..0	2206 11 BC027001
15	402..2	63..3	Mus muscu
16	402..2	63..0	BG06412
17	401..2	62..9	602669744
18	385..4	60..4	A1077609
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20	385..2	60..4	CG55930
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22	354..6	55..6	813 10 A1653400
23	328..6	51..5	13 B131990
24	327..4	51..3	508 13 B131990
25	320..6	50..7	10 BCG33840
26	320..6	50..3	29 CG55930
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			/dev-stages="adult"
			/clone-lib="Homo sapiens ADULT BRAIN"
			/notes="organ: brain; Vector: pCWS190; Fwd: 5' 1st strand cDNA was primed with a multi-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRI sites of the pCWS190 vector. Library was not normalized."
			ORIGIN
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			94..3.. Score 601..8; DB 13; Length 1173;
			Best Local Similarity 98..6%; Pred. No. 6..9e-166;
			Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 0;
			3 ATTCGAGATCCGCGACGAGGAGCTGCTAGCCATCTGAA
			4 CGGAAATCTACCCG 622
			5 BP312970 601073491
			6 B1640197 AGENCOURT
			7 BP558824 CMI-RN024
			8 BP442335 BP442335
			9 CG554707 OST16594
			10 CGT01495 BSM16019
			11 CGC29018 OST1406697
			12 A2A61582 MA87009..r
			13 CB737841 AMGRN001..S
			14 BM195210 LT-H-20D0..
			15 AM259195 um89f03..Y
			16 BM164189 BSM00090
			17 B159882 603247981
			18 AM554274 1190901..r
			19 B1598304 DPEZP686G
			20 A1033934 QZ6C01..X
			21 RS15255 YG74056..r1
			22 A1015793 x101aa12..r
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ALIGNMENTS

On nucleic - nucleic search, using SW model

Run on:

August 24, 2004, 20:02:52

(without alignments)

Title: US-10-022-554A-3
Perfect score: 638
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6623.438 Million cell updates/sec

Scoring table: Oligo NUC

Gapop 60.0, Gapext 60.0

Total number of hits satisfying chosen parameters: 6340544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: GenBank

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41: em_htg_ohter*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match 76.0; Score 485; DB 6; Length 638;

Best Local Similarity 99.5%; Pred. No. 1-2e-350; Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Result Query

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4	434	68.0	638	6 108020:	I08020 Sequence 4	
5	434	68.0	638	6 109138	I09138 Sequence 3	
6	434	68.0	1073	9 BG033697	BC032697 Homo sapiens	
7	434	68.0	2259	9 HSHPFL	X51943 Human mRNA	
8	434	65.5	490	6 AR380845	AR380845 Sequence	
9	418	65.5	490	9 HSATCP	K55778 Human Sequence a	
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12	408	63.9	468	6 AX481449	AX481449 Sequence	
13	408	63.9	8501	6 A49428	A49428 Sequence 1	
14	359	56.3	481	6 108499	108499 Sequence 13	
15	359	56.3	481	6 109297	109297 Sequence 10	
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23	345	54.1	600	6 E26523	E26523 Sugar chain	
24	345	54.1	600	6 E26529	E26529 Sugar chain	
25	345	54.1	630	6 E26524	E26524 Sugar chain	
26	345	54.1	630	6 E26525	E26525 Sugar chain	
27	345	54.1	843	6 E26528	E26528 Sugar chain	
29	258	40.4	540	6 E26511	E26511 Sugar chain	
30	255	40.0	543	6 E38003	E38003 Process for	
31	254	39.8	543	6 238007	238007 Process for	
32	253	39.7	540	6 238002	238002 Process for	
33	241	37.8	540	6 238002	238002 Process for	
34	206	32.3	363	6 AX998995	AX998995 Sequence	
35	206	32.3	363	6 BD044518	BD044518 Sequence	
36	203	31.8	540	6 E38004	E38004 Process for	
37	202	31.7	249	9 HUMPGPAB	I01467 Homo sapiens	
38	195	30.6	503	9 HUMPGFAL	M13490 Human sapiens	
39	195	30.6	1082	9 HUMHCG7L	M23017 Human heparin	
40	195	30.6	76415	9 AC05370	AC05370 Homo sapiens	
C	41	195	30.6	8893	2 AC091822	AC091822 Homo sapiens
C	42	195	30.6	146437	9 AC010493	AC010493 Homo sapiens
C	43	195	30.6	191734	2 AC016560	AC016560 Homo sapiens
C	44	186	29.2	454	6 A00069	A00069 Artificial
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ALIGNMENTS

RESULT	1	102042	LOCUS	102042	DEFINITION	638 bp 5S-DNA	LINEAR	PAT 21-MAY-1993
DEFINITION			ACCESSION	102042	SEQUENCE	5 from Patent US 4869113.		
VERSION			JOURNAL	102042.1	GI	270417		
KEYWORDS			SOURCE					
			ORGANISM	Unknown.				
			UNCLASSIFIED					
REFERENCES	1 (bases 1 to 638)		AUTHORS	Jaye, M., Burgess, M., MacIag, T. and Drohan, M.				
TITLE			RECOMBINANT DNA VECTOR ENCODING HUMAN ENDOTHELIAL CELL GROWTH					
FACTOR			PATENT	US 4869113-A 5 19-SEP-1989;				
JOURNAL			ROTER BIOTECHNOLOGY, INC.; KING OF PRUSSIA, PA					
FEATURES			LOCATION/QUALIFIERS					
SOURCE			1. /organisms="unknown"					
ORIGIN			/mol_types="unassigned DNA"					

Query Match 76.0; Score 485; DB 6; Length 638;
Best Local Similarity 99.5%; Pred. No. 1-2e-350; Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

and is derived by analysis of the total score distribution.

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